

16U 100 PCT.ST25
SEQUENCE LISTING

<110> OriGene Technologies, Inc

<120> NOVEL EXPRESSED GENES

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<151> 2002-04-01

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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tgaccatggg atg cca gag ccg tgg ggg acc gtt tat ttt cta ggc att 469
Met Pro Glu Pro Trp Gly Thr Val Tyr Phe Leu Gly Ile
1 5 10
gct cag gtt ttc agt ttc ttg ttt tcc tgg tgg aat ttg gaa ggg gtc 517
Ala Gln Val Phe Ser Phe Leu Phe Ser Trp Trp Asn Leu Glu Gly Val
15 20 25
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Met Asn Gln Ala Asp Ala Pro Arg Pro Leu Asn Trp Thr Ile Arg Lys
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Leu Cys His Ala Ala Phe Leu Pro Ser Val Arg Leu Leu Lys Ala Gln
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Lys Ser Trp Ile Glu Arg Ala Phe Tyr Lys Arg Glu Cys Val His Ile
65 70 75
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Ile Pro Ser Thr Lys Asp Pro His Arg Cys Cys Cys Gly Arg Leu Ile
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ggc cag cat gtt ggc ctc acc ccc agt atc tcc gtg ctt cag aat gag 757
Gly Gln His Val Gly Leu Thr Pro Ser Ile Ser Val Leu Gln Asn Glu
95 100 105
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Lys Asn Glu Ser Arg Leu Ser Arg Asn Asp Ile Gln Ser Glu Lys Trp
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tcc atc agc aaa cac act caa ctc agc cct acg gat gct ttt ggg acc 853
Ser Ile Ser Lys His Thr Gln Leu Ser Pro Thr Asp Ala Phe Gly Thr
130 135 140

16U 100 PCT.ST25

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cat gcc tct aag tct cga gga aag ata tgc acc ata ggt att gcc ccc His Ala Ser Lys Ser Arg Gly Lys Ile Cys Thr Ile Gly Ile Ala Pro 240 245 250	1189
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cgg cca tac cag acc atg tcc aat ccc atg agc aag ctc act gtt ctc Arg Pro Tyr Gln Thr Met Ser Asn Pro Met Ser Lys Leu Thr Val Leu 270 275 280 285	1285
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160 100 PCT.ST25
450 455 460

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gtt gac gac att tcc cag gag ctg aat cac aat tcc aga gac ttt ggc Val Asp Asp Ile Ser Gln Glu Leu Asn His Asn Ser Arg Asp Phe Gly 690 695 700	2533
cag ctg gct gtg gag ctc ctg gac cag tcc tac aag cag gac gaa cag Gln Leu Ala Val Glu Leu Leu Asp Gln Ser Tyr Lys Gln Asp Glu Gln 705 710 715	2581
ctg gcc atg aaa ctg ctg acg tat gag ctg aag aac tgg agc aac gcc Leu Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala 720 725 730	2629
acg tgc ctg cag ctt gcc gtg gct gcc aaa cac cgc gac ttc atc gcg Thr Cys Leu Gln Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala 735 740 745	2677
cac acg tgc agc cag atg ctg ctc acc gac atg tgg atg ggc cgg ctc His Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu 750 755 760 765	2725
cgc atg cgc aag aac tca ggc ctc aag gta att ctg gga att cta ctt	2773

16U 100 PCT.ST25

Arg Met Arg Lys Asn Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu	770	775	780	
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Pro Pro Ser Ile Leu Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro	785	790	795	
tat atg tct cag gcc cag gaa atc cac ctc caa gag aag gag gca gaa				2869
Tyr Met Ser Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu	800	805	810	
gaa cca gag aag ccc aca aag gaa aaa gag gaa gag gac atg gag ctc				2917
Glu Pro Glu Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu	815	820	825	
aca gca atg ttg gga cga aac aac ggg gag tcc tcc agg aag aag gat				2965
Thr Ala Met Leu Gly Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp	830	835	840	845
gaa gag gaa gtt cag agc aag cac cgg tta atc ccc ctc ggc aga aaa				3013
Glu Glu Glu Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys	850	855	860	
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Ile Tyr Glu Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr	865	870	875	
ctg gcg tat atc gga tac ctg atg ctc ttc aac tat atc gtg tta gtg				3109
Leu Ala Tyr Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val	880	885	890	
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Lys Met Glu Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr	895	900	905	
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Ile Phe Thr Leu Gly Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu	910	915	920	925
cca ggg aag ttg cta cag aaa gtg aag gta tgg ctg cag gag tac tgg				3253
Pro Gly Lys Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp	930	935	940	
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Cys Val Asn Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly	975	980	985	
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Val Asn Lys Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met	990	995	1000	1005
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Ile Asp Met Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met	1010	1015	1020	
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Ser Phe Gly Val Ala Arg Gln Ala Ile Leu Phe Pro Asn Glu Glu	1025	1030	1035	
cca tca tgg aaa ctg gcc aag aac atc ttc tac atg ccc tat tgg				3580
Pro Ser Trp Lys Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp	1040	1045	1050	
atg att tat ggg gaa gtg ttt gcg gac cag ata gac cct ccc tgt				3625
Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Pro Pro Cys	1055	1060	1065	
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Gly Gln Asn Glu Thr Arg Glu Asp Gly Lys Ile Ile Gln Leu Pro	1070	1075	1080	

16U 100 PCT.ST25

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Pro Cys Lys Thr Gly Ala Trp Ile Val Pro Ala Ile Met Ala Cys	
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Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala	
1100 1105 1110	
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Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile Ser Asn Gln	
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Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe His Glu	
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Gly Arg Met Ala Thr Ala Leu Glu Arg Leu Thr Gly Leu Glu Arg	
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gcc gag tcc aac aaa atc cgc tcg agg acc tcg tca gac tgc acg	4300
Ala Glu Ser Asn Lys Ile Arg Ser Arg Thr Ser Ser Asp Cys Thr	
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gac gcc gcc tac att gtc cgt cag agc agc ttc aac agc cag gaa	4345
Asp Ala Ala Tyr Ile Val Arg Gln Ser Ser Phe Asn Ser Gln Glu	
1295 1300 1305	
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Ser His Ser Phe Tyr Ser Val Asn Met Lys Asp Lys Gly Gly Ile	
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Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His	
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1370 1375 1380	

16U 100 PCT.ST25

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1670 1675 1680 16U 100 PCT.ST25

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Ala Asp Ala Pro Arg Pro Leu Asn Trp Thr Ile Arg Lys Leu Cys His
 35 40 45

Ala Ala Phe Leu Pro Ser Val Arg Leu Leu Lys Ala Gln Lys Ser Trp
 50 55 60

Ile Glu Arg Ala Phe Tyr Lys Arg Glu Cys Val His Ile Ile Pro Ser
 65 70 75 80

Thr Lys Asp Pro His Arg Cys Cys Cys Gly Arg Leu Ile Gly Gln His
 85 90 95

Val Gly Leu Thr Pro Ser Ile Ser Val Leu Gln Asn Glu Lys Asn Glu
 100 105 110

Ser Arg Leu Ser Arg Asn Asp Ile Gln Ser Glu Lys Trp Ser Ile Ser
 115 120 125

16U 100 PCT.ST25

Lys His Thr Gln Leu Ser Pro Thr Asp Ala Phe Gly Thr Ile Glu Phe
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Gln Gly Gly Gly His Ser Asn Lys Ala Met Tyr Val Arg Val Ser Phe
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Asp Thr Lys Pro Asp Leu Leu Leu His Leu Met Thr Lys Glu Trp Gln
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Leu Glu Leu Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Asn
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Phe Glu Leu Gln Pro Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile
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Val Glu Asn Gln Glu Asp Leu Ile Gly Arg Asp Val Val Arg Pro Tyr
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His Ser His Phe Ile Leu Ala Asp Asn Gly Thr Thr Gly Lys Tyr Gly
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Ala Glu Val Lys Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln
305 310 315 320

Lys Ile Asn Thr Arg Ile Gly Gln Gly Val Pro Val Val Ala Leu Ile
325 330 335

Val Glu Gly Gly Pro Asn Val Ile Ser Ile Val Leu Glu Tyr Leu Arg
340 345 350

Asp Thr Pro Pro Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala
355 360 365

Ser Asp Ile Leu Ala Phe Gly His Lys Tyr Ser Glu Glu Gly Gly Leu
370 375 380

Ile Asn Glu Ser Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr
385 390 395 400

Phe Thr Tyr Thr Arg Thr Gln Ala Gln His Leu Phe Ile Ile Leu Met
405 410 415

Glu Cys Met Lys Lys Lys Glu Leu Ile Thr Val Phe Arg Met Gly Ser
420 425 430

Glu Gly His Gln Asp Ile Asp Leu Ala Ile Leu Thr Ala Leu Leu Lys
435 440 445

16U 100 PCT.ST25

Gly Ala Asn Ala Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp
 450 455 460

Asn Arg Val Asp Ile Ala Arg Ser Gln Ile Phe Ile Tyr Gly Gln Gln
 465 470 475 480

Trp Pro Val Gly Ser Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
 485 490 495

Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Ser Met
 500 505 510

His Arg Phe Leu Thr Ile Ser Arg Leu Glu Glu Leu Tyr Asn Thr Arg
 515 520 525

His Gly Pro Ser Asn Thr Leu Tyr His Leu Val Arg Asp Val Lys Lys
 530 535 540

Gly Asn Leu Pro Pro Asp Tyr Arg Ile Ser Leu Ile Asp Ile Gly Leu
 545 550 555 560

Val Ile Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
 565 570 575

Lys Arg Phe Arg Thr Leu Tyr His Asn Leu Phe Gly Pro Lys Arg Pro
 580 585 590

Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Ile Pro Leu Arg Arg
 595 600 605

Gly Arg Lys Thr Thr Lys Lys Arg Glu Glu Glu Val Asp Ile Asp Leu
 610 615 620

Asp Asp Pro Glu Ile Asn His Phe Pro Phe Pro Phe His Glu Leu Met
 625 630 635 640

Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Leu Phe Phe Trp
 645 650 655

Gln His Gly Glu Glu Ala Met Ala Lys Ala Leu Val Ala Cys Lys Leu
 660 665 670

Cys Lys Ala Met Ala His Glu Ala Ser Glu Asn Asp Met Val Asp Asp
 675 680 685

Ile Ser Gln Glu Leu Asn His Asn Ser Arg Asp Phe Gly Gln Leu Ala
 690 695 700

Val Glu Leu Leu Asp Gln Ser Tyr Lys Gln Asp Glu Gln Leu Ala Met
 705 710 715 720

Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala Thr Cys Leu
 725 730 735

Gln Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His Thr Cys
 740 745 750

Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg

16U 100 PCT.ST25
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 Lys Asn Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu Pro Pro Ser
 770 775 780
 Ile Leu Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro Tyr Met Ser
 785 790 795 800
 Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro Glu
 805 810 815
 Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala Met
 820 825 830
 Leu Gly Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp Glu Glu Glu
 835 840 845
 Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr Glu
 850 855 860
 Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala Tyr
 865 870 875 880
 Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met Glu
 885 890 895
 Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe Thr
 900 905 910
 Leu Gly Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu Pro Gly Lys
 915 920 925
 Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val Thr
 930 935 940
 Asp Leu Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg Leu
 945 950 955 960
 Gln Asp Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val Asn
 965 970 975
 Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn Lys
 980 985 990
 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met
 995 1000 1005
 Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly
 1010 1015 1020
 Val Ala Arg Gln Ala Ile Leu Phe Pro Asn Glu Glu Pro Ser Trp
 1025 1030 1035
 Lys Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr
 1040 1045 1050
 Gly Glu Val Phe Ala Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn
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16U 100 PCT.ST25

Glu Thr Arg Glu Asp Gly Lys Ile Ile Gln Leu Pro Pro Cys Lys
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Thr Gly Ala Trp Ile Val Pro Ala Ile Met Ala Cys Tyr Leu Leu
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Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn
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Asn Thr Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val Trp Lys
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Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe His Glu Arg Pro Val
 1130 1135 1140

Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met Thr Met Ile Phe
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Gln His Leu Cys Cys Arg Trp Arg Lys His Glu Ser Asp Pro Asp
 1160 1165 1170

Glu Arg Asp Tyr Gly Leu Lys Leu Phe Ile Thr Asp Asp Glu Leu
 1175 1180 1185

Lys Lys Val His Asp Phe Glu Glu Gln Cys Ile Glu Glu Tyr Phe
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Arg Glu Lys Asp Asp Arg Phe Asn Ser Ser Asn Asp Glu Arg Ile
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Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu
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Glu Val Asn Glu Arg Glu His Ser Met Lys Ala Ser Leu Gln Thr
 1235 1240 1245

Val Asp Ile Arg Leu Ala Gln Leu Glu Asp Leu Ile Gly Arg Met
 1250 1255 1260

Ala Thr Ala Leu Glu Arg Leu Thr Gly Leu Glu Arg Ala Glu Ser
 1265 1270 1275

Asn Lys Ile Arg Ser Arg Thr Ser Ser Asp Cys Thr Asp Ala Ala
 1280 1285 1290

Tyr Ile Val Arg Gln Ser Ser Phe Asn Ser Gln Glu Gly Asn Thr
 1295 1300 1305

Phe Lys Leu Gln Glu Ser Ile Asp Pro Ala Gly Glu Glu Thr Met
 1310 1315 1320

Ser Pro Thr Ser Pro Thr Leu Met Pro Arg Met Arg Ser His Ser
 1325 1330 1335

Phe Tyr Ser Val Asn Met Lys Asp Lys Gly Gly Ile Glu Lys Leu
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Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His Arg Ala Thr
 1355 1360 1365

16U 100 PCT.ST25

Ser Ser His Ser Val Ala Lys Glu Pro Lys Ala Pro Ala Ala Pro
 1370 1375 1380
 Ala Asn Thr Leu Ala Ile Val Pro Asp Ser Arg Arg Pro Ser Ser
 1385 1390 1395
 Cys Ile Asp Ile Tyr Val Ser Ala Met Asp Glu Leu His Cys Asp
 1400 1405 1410
 Ile Asp Pro Leu Asp Asn Ser Val Asn Ile Leu Gly Leu Gly Glu
 1415 1420 1425
 Pro Ser Phe Ser Thr Pro Val Pro Ser Thr Ala Pro Ser Ser Ser
 1430 1435 1440
 Ala Tyr Ala Thr Leu Ala Pro Thr Asp Arg Pro Pro Ser Arg Ser
 1445 1450 1455
 Ile Asp Phe Glu Asp Ile Thr Ser Met Asp Thr Arg Ser Phe Ser
 1460 1465 1470
 Ser Asp Tyr Thr His Leu Pro Glu Cys Gln Asn Pro Trp Asp Ser
 1475 1480 1485
 Glu Pro Pro Met Tyr His Thr Ile Glu Arg Ser Lys Ser Ser Arg
 1490 1495 1500
 Tyr Leu Ala Thr Thr Pro Phe Leu Leu Glu Glu Ala Pro Ile Val
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 Lys Ser His Ser Phe Met Phe Ser Pro Ser Arg Ser Tyr Tyr Ala
 1520 1525 1530
 Asn Phe Gly Val Pro Val Lys Thr Ala Glu Tyr Thr Ser Ile Thr
 1535 1540 1545
 Asp Cys Ile Asp Thr Arg Cys Val Asn Ala Pro Gln Ala Ile Ala
 1550 1555 1560
 Asp Arg Ala Ala Phe Pro Gly Gly Leu Gly Asp Lys Val Glu Asp
 1565 1570 1575
 Leu Thr Cys Cys His Pro Glu Arg Glu Ala Glu Leu Ser His Pro
 1580 1585 1590
 Ser Ser Asp Ser Glu Glu Asn Glu Ala Lys Gly Arg Arg Ala Thr
 1595 1600 1605
 Ile Ala Ile Ser Ser Gln Glu Gly Asp Asn Ser Glu Arg Thr Leu
 1610 1615 1620
 Ser Asn Asn Ile Thr Val Pro Lys Ile Glu Arg Ala Asn Ser Tyr
 1625 1630 1635
 Ser Ala Glu Glu Pro Ser Ala Pro Tyr Ala His Thr Arg Lys Ser
 1640 1645 1650
 Phe Ser Ile Ser Asp Lys Leu Asp Arg Gln Arg Asn Thr Ala Ser
 1655 1660 1665

16U 100 PCT.ST25

Leu Arg Asn Pro Phe Gln Arg Ser Lys Ser Ser Lys Pro Glu Gly
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Arg Gly Asp Ser Leu Ser Met Arg Arg Leu Ser Arg Thr Ser Ala
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Phe Gln Ser Phe Glu Ser Lys His Asn
 1700 1705

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Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met
 35 40 45

Arg Lys Asn Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu Pro Pro
 50 55 60

Ser Ile Leu Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro Tyr Met
 65 70 75 80

Ser Gln Ala Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro
 85 90 95

Glu Lys Pro Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala
 100 105 110

Met Leu Gly Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp Glu Glu
 115 120 125

Glu Val Gln Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr
 130 135 140

Glu Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala
 145 150 155 160

Tyr Ile Gly Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met
 165 170 175

Glu Arg Trp Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe
 180 185 190

Thr Leu Gly Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu Pro Gly
 195 200 205

Lys Leu Leu Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val
 210 215 220

Thr Asp Leu Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg
 225 230 235 240

16U 100 PCT.ST25

Leu Gln Asp Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val
 245 250 255

Asn Ile Ile Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn
 260 265 270

Lys Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp
 275 280 285

Met Met Tyr Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly
 290 295 300

Val Ala Arg Gln Ala Ile Leu Phe Pro Asn Glu Glu Pro Ser Trp Lys
 305 310 315 320

Leu Ala Lys Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu
 325 330 335

Val Phe Ala Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn Glu Thr Arg
 340 345 350

Glu Asp Gly Lys Ile Ile Gln Leu Pro Pro Cys Lys Thr Gly Ala Trp
 355 360 365

Ile Val Pro Ala Ile Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu
 370 375 380

Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val
 385 390 395 400

Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile
 405 410 415

Met Thr Phe His Glu Arg Pro Val Leu Pro Pro Pro Leu Ile Ile Phe
 420 425 430

Ser His Met Thr Met Ile Phe Gln His Leu Cys Cys Arg Trp Arg Lys
 435 440 445

His Glu Ser Asp Pro Asp Glu Arg Asp Tyr Gly Leu Lys Leu Phe Ile
 450 455 460

Thr Asp Asp Glu Leu Lys Lys Val His Asp Phe Glu Glu Gln Cys Ile
 465 470 475 480

Glu Glu Tyr Phe Arg Glu Lys Asp Asp Arg Phe Asn Ser Ser Asn Asp
 485 490 495

Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg
 500 505 510

Leu Glu Glu Val Asn Glu Arg Glu His Ser Met Lys Ala Ser Leu Gln
 515 520 525

Thr Val Asp Ile Arg Leu Ala Gln Leu Glu Asp Leu Ile Gly Arg Met
 530 535 540

Ala Thr Ala Leu Glu Arg Leu Thr Gly Leu Glu Arg Ala Glu Ser Asn

Page 23

16U 100 PCT.ST25

Pro Glu Arg Glu Ala Glu Leu Ser His Pro Ser Ser Asp Ser Glu Glu
865 870 875 880

Asn Glu Ala Lys Gly Arg Arg Ala Thr Ile Ala Ile Ser Ser Gln Glu
885 890 895

Gly Asp Asn Ser Glu Arg Thr Leu Ser Asn Asn Ile Thr Val Pro Lys
900 905 910

Ile Glu Arg Ala Asn Ser Tyr Ser Ala Glu Glu Pro Ser Ala Pro Tyr
915 920 925

Ala His Thr Arg Lys Ser Phe Ser Ile Ser Asp Lys Leu Asp Arg Gln
930 935 940

Arg Asn Thr Ala Ser Leu Arg Asn Pro Phe Gln Arg Ser Lys Ser Ser
945 950 955 960

Lys Pro Glu Gly Arg Gly Asp Ser Leu Ser Met Arg Arg Leu Ser Arg
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Thr Ser Ala Phe Gln Ser Phe Glu Ser Lys His Asn
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Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ala Thr Cys Leu Gln Leu
35 40 45

Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His Thr Cys Ser Gln
50 55 60

Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg Lys Asn
65 70 75 80

Ser Gly Leu Lys Val Ile Leu Gly Ile Leu Leu Pro Pro Ser Ile Leu
85 90 95

Ser Leu Glu Phe Lys Asn Lys Asp Asp Met Pro Tyr Met Ser Gln Ala
100 105 110

Gln Glu Ile His Leu Gln Glu Lys Glu Ala Glu Glu Pro Glu Lys Pro
115 120 125

Thr Lys Glu Lys Glu Glu Glu Asp Met Glu Leu Thr Ala Met Leu Gly
130 135 140

Arg Asn Asn Gly Glu Ser Ser Arg Lys Lys Asp Glu Glu Glu Val Gln
145 150 155 160

16U 100 PCT.ST25

Ser Lys His Arg Leu Ile Pro Leu Gly Arg Lys Ile Tyr Glu Phe Tyr
165 170 175

Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Leu Ala Tyr Ile Gly
180 185 190

Tyr Leu Met Leu Phe Asn Tyr Ile Val Leu Val Lys Met Glu Arg Trp
195 200 205

Pro Ser Thr Gln Glu Trp Ile Val Ile Ser Tyr Ile Phe Thr Leu Gly
210 215 220

Ile Glu Lys Met Arg Glu Ile Leu Met Ser Glu Pro Gly Lys Leu Leu
225 230 235 240

Gln Lys Val Lys Val Trp Leu Gln Glu Tyr Trp Asn Val Thr Asp Leu
245 250 255

Ile Ala Ile Leu Leu Phe Ser Val Gly Met Ile Leu Arg Leu Gln Asp
260 265 270

Gln Pro Phe Arg Ser Asp Gly Arg Val Ile Tyr Cys Val Asn Ile Ile
275 280 285

Tyr Trp Tyr Ile Arg Leu Leu Asp Ile Phe Gly Val Asn Lys Tyr Leu
290 295 300

Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met Met Tyr
305 310 315 320

Phe Val Ile Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg
325 330 335

Gln Ala Ile Leu Phe Pro Asn Glu Glu Pro Ser Trp Lys Leu Ala Lys
340 345 350

Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala
355 360 365

Asp Gln Ile Asp Pro Pro Cys Gly Gln Asn Glu Thr Arg Glu Asp Gly
370 375 380

Lys Ile Ile Gln Leu Pro Pro Cys Lys Thr Gly Ala Trp Ile Val Pro
385 390 395 400

Ala Ile Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn
405 410 415

Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile
420 425 430

Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe
435 440 445

His Glu Arg Pro Val Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met
450 455 460

Thr Met Ile Phe Gln His Leu Cys Cys Arg Trp Arg Lys His Glu Ser
465 470 475 480

16U 100 PCT.ST25

Asp Pro Asp Glu Arg Asp Tyr Gly Leu Lys Leu Phe Ile Thr Asp Asp
 485 490 495

Glu Leu Lys Lys Val His Asp Phe Glu Glu Gln Cys Ile Glu Glu Tyr
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Phe Arg Glu Lys Asp Asp Arg Phe Asn Ser Ser Asn Asp Glu Arg Ile
 515 520 525

Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu Glu
 530 535 540

Val Asn Glu Arg Glu His Ser Met Lys Ala Ser Leu Gln Thr Val Asp
 545 550 555 560

Ile Arg Leu Ala Gln Leu Glu Asp Leu Ile Gly Arg Met Ala Thr Ala
 565 570 575

Leu Glu Arg Leu Thr Gly Leu Glu Arg Ala Glu Ser Asn Lys Ile Arg
 580 585 590

Ser Arg Thr Ser Ser Asp Cys Thr Asp Ala Ala Tyr Ile Val Arg Gln
 595 600 605

Ser Ser Phe Asn Ser Gln Glu Gly Asn Thr Phe Lys Leu Gln Glu Ser
 610 615 620

Ile Asp Pro Ala Gly Glu Glu Thr Met Ser Pro Thr Ser Pro Thr Leu
 625 630 635 640

Met Pro Arg Met Arg Ser His Ser Phe Tyr Ser Val Asn Met Lys Asp
 645 650 655

Lys Gly Gly Ile Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu
 660 665 670

Ser Leu His Arg Ala Thr Ser Ser His Ser Val Ala Lys Glu Pro Lys
 675 680 685

Ala Pro Ala Ala Pro Ala Asn Thr Leu Ala Ile Val Pro Asp Ser Arg
 690 695 700

Arg Pro Ser Ser Cys Ile Asp Ile Tyr Val Ser Ala Met Asp Glu Leu
 705 710 715 720

His Cys Asp Ile Asp Pro Leu Asp Asn Ser Val Asn Ile Leu Gly Leu
 725 730 735

Gly Glu Pro Ser Phe Ser Thr Pro Val Pro Ser Thr Ala Pro Ser Ser
 740 745 750

Ser Ala Tyr Ala Thr Leu Ala Pro Thr Asp Arg Pro Pro Ser Arg Ser
 755 760 765

Ile Asp Phe Glu Asp Ile Thr Ser Met Asp Thr Arg Ser Phe Ser Ser
 770 775 780

Asp Tyr Thr His Leu Pro Glu Cys Gln Asn Pro Trp Asp Ser Glu Pro
 785 790 795 800

16U 100 PCT.ST25

Pro Met Tyr His Thr Ile Glu Arg Ser Lys Ser Ser Arg Tyr Leu Ala
805 810 815

Thr Thr Pro Phe Leu Leu Glu Glu Ala Pro Ile Val Lys Ser His Ser
820 825 830

Phe Met Phe Ser Pro Ser Arg Ser Tyr Tyr Ala Asn Phe Gly Val Pro
835 840 845

Val Lys Thr Ala Glu Tyr Thr Ser Ile Thr Asp Cys Ile Asp Thr Arg
850 855 860

Cys Val Asn Ala Pro Gln Ala Ile Ala Asp Arg Ala Ala Phe Pro Gly
865 870 875 880

Gly Leu Gly Asp Lys Val Glu Asp Leu Thr Cys Cys His Pro Glu Arg
885 890 895

Glu Ala Glu Leu Ser His Pro Ser Ser Asp Ser Glu Glu Asn Glu Ala
900 905 910

Lys Gly Arg Arg Ala Thr Ile Ala Ile Ser Ser Gln Glu Gly Asp Asn
915 920 925

Ser Glu Arg Thr Leu Ser Asn Asn Ile Thr Val Pro Lys Ile Glu Arg
930 935 940

Ala Asn Ser Tyr Ser Ala Glu Glu Pro Ser Ala Pro Tyr Ala His Thr
945 950 955 960

Arg Lys Ser Phe Ser Ile Ser Asp Lys Leu Asp Arg Gln Arg Asn Thr
965 970 975

Ala Ser Leu Arg Asn Pro Phe Gln Arg Ser Lys Ser Ser Lys Pro Glu
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Phe Gln Ser Phe Glu Ser Lys His Thr
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35 40 45

Val Pro Ile Met Leu Ser Gln Arg Gly Leu Leu Ala Thr Cys Thr His
50 55 60

16U 100 PCT.ST25

Ser Gly Val Phe Leu Leu Pro Tyr Arg Leu Pro Pro Tyr Thr Gln Leu
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Ala Pro Cys Gly Gln Asn Glu Thr Arg Glu Asp Gly Lys Thr Ile Gln
85 90 95

Leu Pro Pro Cys Lys Thr Gly Ala Trp Ile Val Pro Ala Ile Met Ala
100 105 110

Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala
115 120 125

Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val
130 135 140

Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe His Glu Arg Pro
145 150 155 160

Val Leu Pro Pro Pro Leu Ile Ile Phe Ser His Met Thr Met Ile Phe
165 170 175

Gln His Val Cys Cys Arg Trp Arg Lys His Glu Ser Asp Gln Asp Glu
180 185 190

Arg Asp Tyr Gly Leu Lys Phe Leu Ile Thr Gly Asp Glu Leu Arg Lys
195 200 205

Val His Asp Phe Glu Glu Gln Cys Ile Glu Glu Tyr Phe Arg Glu Lys
210 215 220

Asp Asp Arg Phe Asn Ser Ser Asn Asp Glu Arg Ile Arg Val Thr Ser
225 230 235 240

Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu Glu Val Asn Glu Arg
245 250 255

Glu His Ser Met Lys Ala Ser Leu Gln Thr Val Asp Ile Arg Leu Ala
260 265 270

Gln Leu Glu Asp Leu Ile Gly Arg Met Ala Thr Ala Leu Glu Arg Leu
275 280 285

Thr Gly Leu Glu Arg Ala Glu Ser Asn Lys Ile Arg Ser Arg Thr Ser
290 295 300

Ser Asp Cys Thr Asp Ala Ala Tyr Ile Val Arg Gln Ser Ser Phe Asn
305 310 315 320

Ser Gln Glu Gly Asn Thr Phe Lys Leu Gln Glu Ser Ile Asp Pro Ala
325 330 335

Gly Glu Glu Thr Ile Ser Pro Thr Ser Pro Thr Leu Met Pro Arg Met
340 345 350

Arg Ser His Ser Phe Tyr Ser Val Asn Val Lys Asp Lys Gly Gly Ile
355 360 365

Glu Lys Leu Glu Ser Ile Phe Lys Glu Arg Ser Leu Ser Leu His Arg

370 375 16U 100 PCT.ST25
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Ala Thr Ser Ser His Ser Val Ala Lys Glu Pro Lys Ala Pro Ala Ala
 385 390 395 400

Pro Ala Asn Thr Leu Ala Ile Val Pro Asp Ser Arg Arg Pro Ser Ser
 405 410 415

Cys Ile Asp Ile Tyr Val Ser Ala Met Asp Glu Leu His Cys Asp Ile
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Glu Pro Leu Asp Asn Ser Met Asn Ile Leu Gly Leu Gly Glu Pro Ser
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Phe Ser Ala Leu Ala Pro Ser Thr Thr Pro Ser Ser Ser Ala Tyr Ala
 450 455 460

Thr Leu Ala Pro Thr Asp Arg Pro Pro Ser Arg Ser Ile Asp Phe Glu
 465 470 475 480

Asp Leu Thr Ser Met Asp Thr Arg Ser Phe Ser Ser Asp Tyr Thr His
 485 490 495

Leu Pro Glu Cys Gln Asn Pro Trp Asp Thr Asp Pro Pro Thr Tyr His
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Thr Ile Glu Arg Ser Lys Ser Ser Arg Tyr Leu Ala Thr Thr Pro Phe
 515 520 525

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 530 535 540

Pro Ser Arg Ser Tyr Tyr Ala Asn Phe Gly Val Pro Val Lys Thr Ala
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Glu Tyr Thr Ser Ile Thr Asp Cys Ile Asp Thr Arg Cys Val Asn Ala
 565 570 575

Pro Gln Ala Ile Ala Asp Arg Ala Thr Phe Pro Gly Gly Leu Gly Asp
 580 585 590

Lys Val Glu Asp Leu Ser Cys Cys His Pro Glu Arg Glu Ala Glu Leu
 595 600 605

Ser His Pro Ser Ser Asp Ser Glu Glu Asn Glu Ala Arg Gly Gln Arg
 610 615 620

Ala Ala Asn Pro Ile Ser Ser Gln Glu Ala Glu Asn Ala Asp Arg Thr
 625 630 635 640

Leu Ser Asn Asn Ile Thr Val Pro Lys Ile Glu Arg Ala Asn Ser Tyr
 645 650 655

Ser Ala Glu Glu Pro Asn Val Pro Tyr Ala His Thr Arg Lys Ser Phe
 660 665 670

Ser Ile Ser Asp Lys Leu Asp Arg Gln Arg Asn Thr Ala Ser Leu Arg
 675 680 685

16U 100 PCT.ST25

Asn Pro Phe Gln Arg Lys Thr Ile Leu Gln Tyr Thr Pro Asn Lys Leu
690 695 700

Tyr Pro Glu Cys Leu Leu Ser Ser Ser Thr Gly Ala Val Glu Leu Tyr
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Asp Pro Ala Glu Ala Ile Leu Leu Ala Ala Phe Leu Asp Gly Gly Tyr
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Met Ala Val Gln Gly
1 5

tcc cag aga aga ctt ctg ggc tcc ctc aac tcc acc ccc aca gcc atc 404
Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala Ile
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ccc cag ctg ggg ctg gct gcc aac cag aca gga gcc cgg tgc ctg gag 452
Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu Glu

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ctg gtg agc ggg agc aac gtg ctg gag acg gcc gtc atc ctc ctg ctg Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu Leu Leu 90 95 100			644
gag gcc ggt gca ctg gtg gcc cgg gct gcg gtg ctg cag cag ctg gac Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu Asp 105 110 115			692
aat gtc act gac gtg atc acc tgc agc tcc atg ctg tcc agc ctc tgc Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu Cys 120 125 130			740
ttc ctg ggc gcc atc gcc gtg gac cgc tac atc tcc atc ttc tac gca Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr Ala 135 140 145			788
ctg cgc tac cac agc atc gtg acc ctg ccg cgg gcg cgg cga gcc gtt Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg Ala Val 150 155 160 165			836
gcg gcc atc tgg gtg gcc agt gtc gtc ttc agc acg ctc ttc atc gcc Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala 170 175 180			884
tac tac gac cac gtg gcc gtc ctg ctg tgc ctc gtg gtc ttc ttc ctg Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu 185 190 195		/	932
gct atg ctg gtg ctc atg gcc gtg ctg tac gtc cac atg ctg gcc cgg Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg 200 205 210			980
gcc tgc cag cac gcc cag ggc atc gcc cgg ctc cac aag agg cag cgc Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg 215 220 225			1028
ccg gtc cac cag ggc ttt ggc ctt aaa ggc gct gtc acc ctc acc atc Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile 230 235 240 245			1076
ctg ctg ggc att ttc ttc ctc tgc tgg ggc ccc ttc ttc ctg cat ctc Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu His Leu 250 255 260			1124
aca ctc atc gtc ctc tgc ccc gag cac ccc acg tgc ggc tgc atc ttc Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile Phe 265 270 275			1172
aag aac ttc aac ctc ttt ctc gcc ctc atc atc tgc aat gcc atc atc Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile Ile 280 285 290			1220
gac ccc ctc atc tac gcc ttc cac agc cag gag ctc cgc agg acg ctc Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr Leu 295 300 305			1268
aag gag gtg ctg aca tgc tcc tgc tct cag gac cgt gcc ctc gtc agc Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp Arg Ala Leu Val Ser 310 315 320 325			1316
tgg gat gtg aag tct ctg ggt gga agt gtg tgc caa gag cta ctc cca Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys Gln Glu Leu Leu Pro 330 335 340			1364
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16U 100 PCT.ST25

Gln	Gln	Pro	Gln	Glu	Lys	Gly	Leu	Cys	Asp	Gln	Lys	Ala	Ser	Ser	Thr	
345								350					355			
gcc ttg cag cgg ctc ctg caa aag gag cct aga gga agg acg agc agg	1460															
Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg Gly Arg Thr Ser Arg																
360 365 370																
tgc agc agg gcc cca gtc ccc tcc act ctt gac gct gtc cta gct gca	1508															
Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp Ala Val Leu Ala Ala																
375 380 385																
gaa gag gcg ggt tcc cag cct tcc ctg tgaccacatg tgacctcagc	1555															
Glu Glu Ala Gly Ser Gln Pro Ser Leu																
390 395																
cgggacacat ccctttgctg gccctggccc tgagtccctc cagccatgat gagccgtgaa	1615															
tgggaccatc cctgtccact ctgagatgcc tggaaggggg ctgagtgcag agactgagca	1675															
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ctacgcaggc tcagtcagca gccccctggc cagccccacc cctgactgcc ggcctcagaa	1795															
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attctggtgg acctggaacc cggaaccatg gacagtgtcc gctcaggggc ctttgacat	2035															
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ggtcactaca cggagggggc ggagctgggt gattcgggtcc tggatgtggt gcggaaggag	2155															
tgtgaaaact gcgactgcct gcaggggctt cagctgaccc actcgtctgg gggcggcacg	2215															
ggctccggca tgggcacgtt gctcatcagc aagggtgcgtg aggagtatcc cgaccgcatc	2275															
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aacgccacgc tgtccatcca ccagctggtg gagaacacgg atgagacctt ctgcatcgac	2395															
aacgagggcg tctacgacat ctgcttcctc accctcaagc tggccacgcc cacctacggg	2455															
gacctcaacc acctggtatc ggccaccatg agcggagtca ccacctcctt gcgcttcccg	2515															
ggccagctca acgctgacct gcgcaagctg gccgtcaaca tgggtgccctt cccgcgcctg	2575															
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gacccgcgcc acggccgcta cctgacggtg gccaccgtgt tccggggccg catgtccatg	2755															
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cagttcacgg ccatgttccg gcgcaaggcc ttcctgcact ggtacacggg cgagggcatg	2995															
gacgagatgg agttcaccca ggccgagagc aacatgaacg acctggtgtc cgagtaccag	3055															
cagtaccagg acgccacggc cgaggaagag ggccgagatgt acgaagacga cgaggaggag	3115															
tcggaggccc agggccccaa gtgaagctgc tcgcagctgg agtgagaggc aggtggcggc	3175															
cggggccgaa gccagcagtg tctaaacccc cgagagccatc ttgctgccga caccctgctt	3235															
tcccctcgcc ctagggtctc cttgccgccc tcctgcagta tttatggcct cgtcctcccc	3295															
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16U 100 PCT.ST25

<210> 26
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 26

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
 1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

16U 100 PCT.ST25

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 27
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 27

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Thr Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

16U 100 PCT.ST25

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 28
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

16U 100 PCT.ST25

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
370 375 380

16U 100 PCT.ST25

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 29
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 29

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

16U 100 PCT.ST25

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Pro Arg
 355 360 365

Gly Arg Thr Ser Arg Cys Ser Arg Ala Pro Val Pro Ser Thr Leu Asp
 370 375 380

Ala Val Leu Ala Ala Glu Glu Ala Gly Ser Gln Pro Ser Leu
 385 390 395

<210> 30
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
 1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
 115 120 125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

16U 100 PCT.ST25

Ala Arg Gln Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
305 310 315

<210> 31
<211> 382
<212> PRT
<213> Homo sapiens

<400> 31

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Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100 105 110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115 120 125

16U 100 PCT.ST25

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160

Ala Arg Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175

Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Cys Ser Gln Asp
 305 310 315 320

Arg Ala Leu Val Ser Trp Asp Val Lys Ser Leu Gly Gly Ser Val Cys
 325 330 335

Gln Glu Leu Leu Pro Gln Gln Pro Gln Glu Lys Gly Leu Cys Asp Gln
 340 345 350

Lys Ala Ser Ser Thr Ala Leu Gln Arg Leu Leu Gln Lys Glu Val Lys
 355 360 365

Ser Leu Pro Gln Ala Lys Gly Pro Gly Leu Gln Glu Pro Pro
 370 375 380

<210> 32
 <211> 22
 <212> DNA
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<400> 32
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22

<210> 33
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 <212> DNA
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16U 100 PCT.ST25

<400> 33
gctcgtcctt cctctaggct cc 22

<210> 34
<211> 22
<212> DNA
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<400> 34
aggaagcagc tcccagttct ga 22

<210> 35
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<212> DNA
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<400> 35
cttccgcagc ggaaatggcg cgccgcccg ggagggcggg agcagcgccc 50

<210> 36
<211> 50
<212> DNA
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cctcaggctc tacaagatgc ctgaaaacac caacctctcc agggctcact 50

<210> 37
<211> 50
<212> DNA
<213> Homo sapiens

<400> 37
aacgactttt taaaacgcag agaaaagctc cattcttccc aggacctcag 50

<210> 38
<211> 7062
<212> DNA
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<222> (186)..(5288)
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<400> 38
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cctagcacca cagacttata cttcgcctgc actttccgtc tttcttctct gggcgccac 180
caaca atg gat ggc aac tcc ctg ctc tcg gta cca agc aac ttg gag tca 230
Met Asp Gly Asn Ser Leu Leu Ser Val Pro Ser Asn Leu Glu Ser
1 5 10 15
tca cgg atg tat gac gtt ttg gaa ccg cag cag ggc aga ggc tgt ggc 278
Ser Arg Met Tyr Asp Val Leu Glu Pro Gln Gln Gly Arg Gly Cys Gly
20 25 30
agc tca gga agc ggc ccg ggg aac tcc atc aca gcc tgt aag aag gtt 326
Ser Ser Gly Ser Gly Pro Gly Asn Ser Ile Thr Ala Cys Lys Lys Val
35 40 45
ctt cgc agc aat agc ctg ctg gag tca aca gac tac tgg ttg cag aat 374
Leu Arg Ser Asn Ser Leu Leu Glu Ser Thr Asp Tyr Trp Leu Gln Asn
50 55 60
cag agg atg ccc tgc caa att ggt ttt gta gaa gac aag tct gaa aac 422
Gln Arg Met Pro Cys Gln Ile Gly Phe Val Glu Asp Lys Ser Glu Asn
65 70 75
tgt gct tct gtc tgc ttt gtg aat ctt gat gtg aac aag gat gaa tgc 470

16U 100 PCT.ST25

Cys Ala Ser Val Cys Phe Val Asn Leu Asp Val Asn Lys Asp Glu Cys	80	85	90	95	
agc aca gag cac ctg caa cag aaa ctg gtc aac gtt tca cca gat ctt					518
Ser Thr Glu His Leu Gln Gln Lys Leu Val Asn Val Ser Pro Asp Leu		100	105	110	
cca aaa ctt atc agt tcc atg aat gtc caa caa cca aaa gaa aat gaa					566
Pro Lys Leu Ile Ser Ser Met Asn Val Gln Gln Pro Lys Glu Asn Glu		115	120	125	
att gtt gtc cta agt ggg tta gcc tct gga aat ctc cag gca gat ttt					614
Ile Val Val Leu Ser Gly Leu Ala Ser Gly Asn Leu Gln Ala Asp Phe		130	135	140	
gaa gtt tca cag tgc cct tgg ctg cca gat atc tgc ttg gtc caa tgt					662
Glu Val Ser Gln Cys Pro Trp Leu Pro Asp Ile Cys Leu Val Gln Cys		145	150	155	
gca aga ggg aac aga cca aac agt acc aac tgc atc atc ttt gaa atc					710
Ala Arg Gly Asn Arg Pro Asn Ser Thr Asn Cys Ile Ile Phe Glu Ile		160	165	170	175
aac aaa ttt ctg att ggt ctg gaa ctg gtg cag gag cga cag ctc cac					758
Asn Lys Phe Leu Ile Gly Leu Glu Leu Val Gln Glu Arg Gln Leu His		180	185	190	
ctg gaa aca aac atc ttg aaa ctg gag gat gac acg aac tgt tcc tta					806
Leu Glu Thr Asn Ile Leu Lys Leu Glu Asp Asp Thr Asn Cys Ser Leu		195	200	205	
tct tca atc gag gaa gac ttt ctc acc gct tct gag cac ttg gag gag					854
Ser Ser Ile Glu Glu Asp Phe Leu Thr Ala Ser Glu His Leu Glu Glu		210	215	220	
gaa agc gag gtg gat gaa tct agg aac gat tat gaa aat ata aat gtc					902
Glu Ser Glu Val Asp Glu Ser Arg Asn Asp Tyr Glu Asn Ile Asn Val		225	230	235	
tca gcc aat gtt ttg gaa agt aaa cag cta aag gga gcc acc cag gtg					950
Ser Ala Asn Val Leu Glu Ser Lys Gln Leu Lys Gly Ala Thr Gln Val		240	245	250	255
gaa tgg aat tgc aac aag gaa aag tgg ctt tat gct ttg gaa gac aaa					998
Glu Trp Asn Cys Asn Lys Glu Lys Trp Leu Tyr Ala Leu Glu Asp Lys		260	265	270	
tac atc aac aaa tat ccc aca cca ttg att aaa aca gaa cga tct cca					1046
Tyr Ile Asn Lys Tyr Pro Thr Pro Leu Ile Lys Thr Glu Arg Ser Pro		275	280	285	
gaa aac cta aca aag aac aca gcc ttg cag agt cta gat ccc tca gcc					1094
Glu Asn Leu Thr Lys Asn Thr Ala Leu Gln Ser Leu Asp Pro Ser Ala		290	295	300	
aag cca tca cag tgg aaa aga gaa gct gtg ggg aat ggg aga caa gcc					1142
Lys Pro Ser Gln Trp Lys Arg Glu Ala Val Gly Asn Gly Arg Gln Ala		305	310	315	
aca cat tat tat cat tca gaa gct ttt aaa ggt caa atg gaa aaa tca					1190
Thr His Tyr Tyr His Ser Glu Ala Phe Lys Gly Gln Met Glu Lys Ser		320	325	330	335
cag gca ctg tat att cca aaa gat gct tat ttc tcc atg atg gat aaa					1238
Gln Ala Leu Tyr Ile Pro Lys Asp Ala Tyr Phe Ser Met Met Asp Lys		340	345	350	
gat gta cct tct gca tgt gct gtg gca gag cag aga agc aac cta aac					1286
Asp Val Pro Ser Ala Cys Ala Val Ala Glu Gln Arg Ser Asn Leu Asn		355	360	365	
cca gga gac cat gaa gac aca aga aac gct ctc cct cct aga caa gat					1334
Pro Gly Asp His Glu Asp Thr Arg Asn Ala Leu Pro Pro Arg Gln Asp		370	375	380	
gga gaa gtc acc act ggc aag tat gct aca aat tta gca gaa tcc gtg					1382
Gly Glu Val Thr Thr Gly Lys Tyr Ala Thr Asn Leu Ala Glu Ser Val		385	390	395	

16U 100 PCT.ST25

ctg cag gat gca ttt att aga tta tct caa tct cag tcc aca tta ccc Leu Gln Asp Ala Phe Ile Arg Leu Ser Gln Ser Gln Ser Thr Leu Pro 400 405 410 415	1430
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tgc tat tcc aca aaa gat aca gtg gtt tct cgg tca tgg aat gag ctc Cys Tyr Ser Thr Lys Asp Thr Val Val Ser Arg Ser Trp Asn Glu Leu 435 440 445	1526
ccc aaa atc gtc gtt gtt cag agt cca gat ggc agt gat gct gcc cca Pro Lys Ile Val Val Val Gln Ser Pro Asp Gly Ser Asp Ala Ala Pro 450 455 460	1574
cag cca ggc atc tcc tcc tgg cct gag atg gaa gtc tct gtt gaa acc Gln Pro Gly Ile Ser Ser Trp Pro Glu Met Glu Val Ser Val Glu Thr 465 470 475	1622
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acc ctg tgc tca gaa aat gtc gtc agg aat gaa ctg gca cat acc ctg Thr Leu Cys Ser Glu Asn Val Val Arg Asn Glu Leu Ala His Thr Leu 660 665 670	2198
tcc aat gtt atc ctg agg cat tcc att gat gaa gtt cac cac aaa aat Ser Asn Val Ile Leu Arg His Ser Ile Asp Glu Val His His Lys Asn 675 680 685	2246
atg ata atc gac ccc aat gac aac agg cat tca tct gaa att ctg gac Met Ile Ile Asp Pro Asn Asp Asn Arg His Ser Ser Glu Ile Leu Asp 690 695 700	2294
acc tta atg gaa agt aca aat caa ctg ctt tta gat gtg ata tgc ttc Thr Leu Met Glu Ser Thr Asn Gln Leu Leu Leu Asp Val Ile Cys Phe 705 710 715	2342

16U 100 PCT.ST25

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cag cca tct gat ccg ggt gct agt caa gct tgg aca aaa gcc act gaa Gln Pro Ser Asp Pro Gly Ala Ser Gln Ala Trp Thr Lys Ala Thr Glu 755 760 765	2486
tcc tcc agc agc tct cca ctt agc aat tca cac aac acg agt ctt gtc Ser Ser Ser Ser Ser Pro Leu Ser Asn Ser His Asn Thr Ser Leu Val 770 775 780	2534
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gtg agg cca ggc ctc ttc aag aac ccc acg ctg cag tca caa tta tca Val Arg Pro Gly Leu Phe Lys Asn Pro Thr Leu Gln Ser Gln Leu Ser 800 805 810 815	2630
cgt agt cac aga gtg ccc gat tct tca act gct aca aca tcc tcc aag Arg Ser His Arg Val Pro Asp Ser Ser Thr Ala Thr Thr Ser Ser Lys 820 825 830	2678
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cac agt gag aat gaa tgc aga gcc tct tcc gaa gga caa agg tcc cca His Ser Glu Asn Glu Cys Arg Ala Ser Ser Glu Gly Gln Arg Ser Pro 850 855 860	2774
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gct caa tcc acg ctt caa aca aag cat cca gac atc tac tgc att aca Ala Gln Ser Thr Leu Gln Thr Lys His Pro Asp Ile Tyr Cys Ile Thr 915 920 925	2966
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1025	1030	16U 100 PCT.ST25 1035	
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16U 100 PCT.ST25														
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160 100 PCT.ST25

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16U 100 PCT.ST25

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7062

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Arg Met Pro Cys Gln Ile Gly Phe Val Glu Asp Lys Ser Glu Asn Cys
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Ala Ser Val Cys Phe Val Asn Leu Asp Val Asn Lys Asp Glu Cys Ser
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Thr Glu His Leu Gln Gln Lys Leu Val Asn Val Ser Pro Asp Leu Pro
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Lys Leu Ile Ser Ser Met Asn Val Gln Gln Pro Lys Glu Asn Glu Ile
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Val Val Leu Ser Gly Leu Ala Ser Gly Asn Leu Gln Ala Asp Phe Glu
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Arg Gly Asn Arg Pro Asn Ser Thr Asn Cys Ile Ile Phe Glu Ile Asn
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Lys Phe Leu Ile Gly Leu Glu Leu Val Gln Glu Arg Gln Leu His Leu
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 195 200 205

Ser Ile Glu Glu Asp Phe Leu Thr Ala Ser Glu His Leu Glu Glu Glu
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Ser Glu Val Asp Glu Ser Arg Asn Asp Tyr Glu Asn Ile Asn Val Ser
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Ala Asn Val Leu Glu Ser Lys Gln Leu Lys Gly Ala Thr Gln Val Glu
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Trp Asn Cys Asn Lys Glu Lys Trp Leu Tyr Ala Leu Glu Asp Lys Tyr
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16U 100 PCT.ST25

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16U 100 PCT.ST25

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Pro Asn Thr Gln Glu Lys Tyr Asn Cys Ala Thr Ser Arg Ile Asn Glu
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Val Gln Val Asn Leu Ser Leu Leu Gly Asp Asp Leu Leu Leu Pro Ala
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Cys Ser Glu Asn Val Val Arg Asn Glu Leu Ala His Thr Leu Ser Asn
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Val Ile Leu Arg His Ser Ile Asp Glu Val His His Lys Asn Met Ile

Page 55

160 100 PCT.ST25

Lys His Lys Pro Pro Arg Leu Ser Glu Ile Lys Arg Lys Thr Asp Glu
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16U 100 PCT.ST25

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Ser	Gly	Gln	Gln	Gly	Phe	Gln	Gly	Leu	Ile	Gly	Val	Gln	Gln	Pro	Pro		
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Gln	Ser	Gln	Asn	Val	Ile	Asn	Asn	Gln	Gln	Gly	Thr	Pro	Val	Gln	Ser		
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gtg	atg	gtt	tcc	tac	cca	aca	atg	tct	tct	tat	cag	gtg	cca	atg	acc	2547	
Val	Met	Val	Ser	Tyr	Pro	Thr	Met	Ser	Ser	Tyr	Gln	Val	Pro	Met	Thr		
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Gln	Gly	Ser	Gln	Gly	Leu	Pro	Gln	Gln	Ser	Tyr	Gln	Gln	Pro	Ile	Met		
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cta	cct	aac	cag	gca	ggt	caa	ggg	tca	ctc	cca	gcc	act	gga	atg	cct	2643	
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16U 100 PCT.ST25

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att ggc cca cac tgc ccc tcc agc act gtc cca gtg atg tca gct agc 2739
Ile Gly Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser Ala Ser
815 820 825 830

tgc aga aca aac tgt gca agt atg agc aat gct ggt tgg cag gtc aaa 2787
Cys Arg Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln Val Lys
835 840 845

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Phe

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35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
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Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
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Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
85 90 95

Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
100 105 110

Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
115 120 125

Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
130 135 140

Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn

145 150 155 160 100 PCT.ST25 160

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180 185 190

Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
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Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
210 215 220

Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
225 230 235 240

Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
245 250 255

Ser Ser Ile Asp Lys Glu Asp Asn Gln Gln Asn Arg Met His Pro Phe
260 265 270

Arg Asp Asp Arg Arg Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr
275 280 285

Gln Arg Val Arg Glu Arg Ile Phe Ala His Asp Ser Val Cys Ser Gln
290 295 300

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Cys Asn Glu Thr Tyr Lys Lys Arg Gln Leu Phe Arg Gly Asn Arg Asp
325 330 335

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Leu Lys Trp Ser Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp
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Gly Gly Ile Thr Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg
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Pro Glu Asn Gly Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr
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16U 100 PCT.ST25

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Gln Tyr Pro Ala Val Ser Phe Pro Pro Gln His Leu Leu Pro Val Ser
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Pro Thr Gln His Phe Pro Met Arg Asp Asp Val Ala Thr Gln Phe Gly
580 585 590

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Ser Gly Pro Val Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln
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Pro Ser Tyr Val Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly
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Pro Ser Pro Gln Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro
660 665 670

Val Tyr Tyr Tyr Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln
675 680 685

Tyr Arg Pro Met Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln
690 695 700

Met Pro Gln Ala Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly
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Gln Gln Gly Phe Gln Gly Leu Ile Gly Val Gln Gln Pro Pro Gln Ser
725 730 735

Gln Asn Val Ile Asn Asn Gln Gln Gly Thr Pro Val Gln Ser Val Met
740 745 750

Val Ser Tyr Pro Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly
755 760 765

Ser Gln Gly Leu Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro
770 775 780

16U 100 PCT.ST25

Asn Gln Ala Gly Gln Gly Ser Leu Pro Ala Thr Gly Met Pro Val Tyr
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Cys Asn Val Thr Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly
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Pro His Cys Pro Ser Ser Thr Val Pro Val Met Ser Ala Ser Cys Arg
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Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln Val Lys Phe
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 Met Ser Glu Gln Gly Asp Leu Asn
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 Gln Ala Ile Ala Glu Glu Gly Gly Thr Glu Gln Glu Thr Ala Thr Pro
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 25 30 35 40
 gaa ctg cag agg cgg ctg gag gct cag aat caa gaa aga aga aaa tcc 496
 Glu Leu Gln Arg Arg Leu Glu Ala Gln Asn Gln Glu Arg Arg Lys Ser
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 Lys Ser Gly Ala Gly Lys Gly Lys Leu Thr Arg Ser Leu Ala Val Cys
 60 65 70
 gag gaa tct tct gcc aga cca gga ggt gaa agt ctt cag gat cag gaa 592
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 75 80 85
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 Ser Ile His Leu Gln Leu Ser Ser Phe Ser Ser Leu Gln Glu Glu Asp
 90 95 100
 aaa tct agg aaa gat gac tct gaa aga gaa aaa gaa aag gat aaa aac 688
 Lys Ser Arg Lys Asp Asp Ser Glu Arg Glu Lys Glu Lys Asp Lys Asn
 105 110 115 120
 aaa gat aaa acc tct gaa aaa ccc aag atc aga atg tta tca aaa gat 736
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 125 130 135
 tgc agc caa gaa tac acg gat tct aca ggc ata gac tta cac gag ttt 784
 Cys Ser Gln Glu Tyr Thr Asp Ser Thr Gly Ile Asp Leu His Glu Phe
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tat aaa aag ttc cct cag atg tca tcg tat cag agg atg ctt gtc cat	928
Tyr Lys Lys Phe Pro Gln Met Ser Ser Tyr Gln Arg Met Leu Val His	
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cga gtg gca gct tat ttt gga ttg gat cac aat gtg gat caa aca gga	976
Arg Val Ala Ala Tyr Phe Gly Leu Asp His Asn Val Asp Gln Thr Gly	
205 210 215	
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Lys Ser Val Ile Ile Asn Lys Thr Ser Ser Thr Arg Ile Pro Glu Gln	
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Arg Phe Cys Glu His Leu Lys Asp Glu Lys Gly Glu Ser Gln Lys	
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Ile Glu Glu Arg Glu Glu Tyr Gln Arg Val Arg Glu Arg Ile Phe	
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Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu Ala Ala Thr Gly Ile Pro	
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745 750 755 760															
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16U 100 PCT.ST25

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Ala Ser Cys Arg Thr Asn Cys Ala Ser Met Ser Asn Ala Gly Trp Gln
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gtc aaa ttc tga gagctctggc tgtggtacat ttcttcagat atttctcatg 2852
Val Lys Phe
825

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Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
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Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
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Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
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Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
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Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
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Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
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Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn
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160 100 PCT.ST25

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Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
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Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
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Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
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Ser Ser Ile Asp Lys Glu Asp Asn Gln Gln Asn Arg Met His Pro Phe
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Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
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His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
465 470 475 480

16U 100 PCT.ST25

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Gly Pro Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln
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Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr
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Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met
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Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala
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Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu
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Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly
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Arg Phe Cys Glu His Leu Lys Asp Glu Lys Gly Glu Glu Ser Gln Lys	
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16U 100 PCT.ST25

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16U 100 PCT.ST25

810

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16U 100 PCT.ST25

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16U 100 PCT.ST25

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Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
 85 90 95

Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
 100 105 110

Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
 115 120 125

Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
 130 135 140

Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn
 145 150 155 160

Ser Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp
 165 170 175

Phe Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser
 180 185 190

Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
 195 200 205

Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
 210 215 220

Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
 225 230 235 240

Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
 245 250 255

Ser Ser Ile Asp Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser
 260 265 270

Leu Phe Val Glu Asn Arg Gly Asn Arg Asp Gly Ser Gly Arg Thr Ser
 275 280 285

16U 100 PCT.ST25

Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser Asp His
 290 295 300

Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg Asn Leu
 305 310 315 320

Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr Val Leu
 325 330 335

Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys Leu Ser
 340 345 350

Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly Ser Leu
 355 360 365

Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu Val Ser Gly Val
 370 375 380

Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly Ile Gly
 385 390 395 400

Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu
 405 410 415

Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro His Thr
 420 425 430

Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr Asn Pro
 435 440 445

Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln Ser Gln
 450 455 460

Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Val
 465 470 475 480

Gln Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Ser Val
 485 490 495

Gln Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala Val Ser
 500 505 510

Phe Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His Phe Pro
 515 520 525

Met Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu Ser Arg
 530 535 540

Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val Tyr Pro
 545 550 555 560

Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val Ile Ala
 565 570 575

Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser Gly Pro
 580 585 590

Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln Gly Phe

16U 100 PCT.ST25
605

595 600

Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr Pro Ser
610 615 620

Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met Ala Pro
625 630 635 640

Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala Ala Gln
645 650 655

Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly
660 665 670

Leu Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile Asn Asn
675 680 685

Gln Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro Thr Met
690 695 700

Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu Pro Gln
705 710 715 720

Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly Gln Gly
725 730 735

Ser Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro
740 745 750

Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro Ser Ser
755 760 765

Thr Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala Ser Met
770 775 780

Ser Asn Ala Gly Trp Gln Val Lys Phe
785 790

<210> 51
<211> 1006
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (280)..(549)
<223>

<400> 51
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cattagtgtt gacgatgtgt cacactgtgt aagggaatcg catggagatg ggcattccga 120
actgttaatg gggacatggg actccagttg tctctgatca cttgtgtgga ttttcctggc 180
gtagaacgac agaagccgct agtaagtcgc caagacctac agcaggaatt ctgcaccaaa 240
gggcataaaa tcttgttatt ttaatttgca tctgggaga atg tct gag caa gga 294
Met Ser Glu Gln Gly
1 5
gac ctg aat cag gca ata gca gag gaa gga ggg act gag cag gag acg 342
Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly Thr Glu Gln Glu Thr 20
10 15 20
gcc act cca gag aac ggc att gtt aaa tca gaa agt ctg gat gaa gag 390

16U 100 PCT.ST25

Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu Ser Leu Asp Glu Glu
 25 30 35

gag aaa ctg gaa ctg cag agg cgg ctg gag gct cag aat caa gaa aga 438
 Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala Gln Asn Gln Glu Arg
 40 45 50

aga aaa tcc aag tca gga gca gga aaa ggt aaa ctg act cgc agt ctt 486
 Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys Leu Thr Arg Ser Leu
 55 60 65

gct gtc tgt gag gaa tct tct gcc aga cca gga ggt gaa agt ctt cag 534
 Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly Gly Glu Ser Leu Gln
 70 75 80 85

gat cag act ctc tga aaactgcaaa tggaaaggaa ttcaaaagaa tttagattaa 589
 Asp Gln Thr Leu

aagttaaata aaaagtaggc acagtagtgc tgaattttcc tcaaaggctc tcttttgata 649
 aggtgaacc aaatataatc ccaagtatcc tctctccttc cttgttgag atgtcttacc 709
 tctcagctcc caaaatgcac ttgcctataa gaaacacaat tgctggttca tatgaaactt 769
 wagaatatgt gaataagggt catttaactt tggagaaata cttttatgsc tttggtggag 829
 atttctcaat actgcaaaag ttgtccagaa atgaatctga gctgatggtg actttaagtt 889
 aatattatta atatatcact gcatattttt acccttattt ttgctcctta cagcaagatt 949
 agtaggttat aaaaatttaa atttaaacaa aattatttca tgacaaaatg ggaaact 1006

<210> 52
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 52

Met Ser Glu Gln Gly Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly
 1 5 10 15

Thr Glu Gln Glu Thr Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu
 20 25 30

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Thr Leu
 85

<210> 53
 <211> 807
 <212> PRT
 <213> Mus musculus

<400> 53

Met Ser Glu Gln Gly Gly Leu Thr Pro Thr Ile Leu Glu Glu Gly Gln
 1 5 10 15

Thr Glu Pro Glu Ser Ala Pro Glu Asn Gly Ile Leu Lys Ser Glu Ser
 20 25 30

16U 100 PCT.ST25

Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Ala Ala Gln
 35 40 45

Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys Leu
 50 55 60

Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Ser Gly Gly
 65 70 75 80

Glu Ser His Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser Phe
 85 90 95

Pro Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu Arg
 100 105 110

Glu Lys Glu Lys Asp Lys Asn Arg Glu Lys Leu Ser Glu Arg Pro Lys
 115 120 125

Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser Thr
 130 135 140

Gly Ile Asp Leu His Gly Phe Leu Ile Asn Thr Leu Lys Asn Asn Ser
 145 150 155 160

Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Met Ile Asp Phe
 165 170 175

Ile Ala Asp Ser Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser
 180 185 190

Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp
 195 200 205

His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser
 210 215 220

Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu
 225 230 235 240

Lys Ser Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser
 245 250 255

Ser Ile Asp Lys Glu Asp Asn Gln Asn Arg Met His Pro Phe Arg Asp
 260 265 270

Asp Arg Arg Ser Lys Ser Ile Glu Glu Arg Glu Glu Glu Tyr Gln Arg
 275 280 285

Val Arg Glu Arg Ile Phe Ala His Asp Ser Val Cys Ser Gln Glu Ser
 290 295 300

Leu Phe Leu Asp Asn Ser Arg Leu Gln Glu Asp Met His Ile Cys Asn
 305 310 315 320

Glu Thr Tyr Lys Lys Arg Gln Leu Phe Arg Ala His Arg Asp Ser Ser
 325 330 335

Gly Arg Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Thr Glu Leu Arg
 340 345 350

16U 100 PCT.ST25

Trp Pro Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser
 355 360 365

Asn Arg Asn Leu Lys Pro Thr Met Thr Lys Thr Ala Ser Phe Gly Gly
 370 375 380

Ile Thr Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Ala
 385 390 395 400

Gly Lys Leu Ser Lys Thr Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser
 405 410 415

Ser Gly Ser Leu Ser Arg Thr His Pro Gln Ser Thr Ala Leu Thr Ser
 420 425 430

Ser Val Ala Ala Gly Ser Pro Gly Cys Met Ala Tyr Ser Glu Asn Gly
 435 440 445

Met Gly Gly Gln Val Pro Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro
 450 455 460

Leu Glu Ser Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
 465 470 475 480

His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
 485 490 495

Asn Pro Pro Gly Ser Gln Gln Thr Leu Arg Gly Thr Val Gly Gly Gln
 500 505 510

Pro Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Gln
 515 520 525

Val Gln Ala Ser Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Arg
 530 535 540

Glu Glu Leu Ala Ala Gln Phe Ser Gln Leu Ser Met Ser Arg Gln Ser
 545 550 555 560

Ser Gly Asp Thr Pro Glu Pro Pro Ser Gly Thr Val Tyr Pro Ala Ser
 565 570 575

Leu Leu Pro Gln Thr Ala Gln Pro Gln Ser Tyr Val Ile Thr Ser Ala
 580 585 590

Gly Gln Gln Leu Ser Thr Gly Gly Phe Ser Asp Ser Gly Pro Pro Ile
 595 600 605

Ser Gln Gln Val Leu Gln Ala Pro Pro Ser Pro Gln Gly Phe Val Gln
 610 615 620

Gln Pro Pro Pro Ala Gln Met Ser Val Tyr Tyr Tyr Pro Ser Gly Gln
 625 630 635 640

Tyr Pro Thr Ser Thr Ser Gln Gln Tyr Arg Pro Leu Ala Ser Val Gln
 645 650 655

Tyr Ser Ala Gln Arg Ser Gln Gln Ile Pro Gln Thr Thr Gln Gln Ala

16U 100 PCT.ST25
660 665 670

Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly Met Met
675 680 685

Gly Val Gln Gln Ser Ala His Ser Gln Gly Val Met Ser Ser Gln Gln
690 695 700

Gly Ala Pro Val His Gly Val Met Val Ser Tyr Pro Thr Met Ser Ser
705 710 715 720

Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Ala Val Pro Gln Gln Thr
725 730 735

Tyr Gln Pro Pro Ile Met Leu Pro Ser Gln Ala Gly Gln Gly Ser Leu
740 745 750

Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro Asn Pro
755 760 765

Gln Asn Asn Leu Arg Leu Met Gly Pro His Cys Pro Ser Ser Thr Val
770 775 780

Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Gly Asn Val Ser Asn
785 790 795 800

Ala Gly Trp Gln Val Lys Phe
805

<210> 54
<211> 648
<212> PRT
<213> Homo sapien

<400> 54

Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp Phe Ile Ala Asp
1 5 10 15

Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser Tyr Gln Arg
20 25 30

Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp His Asn Val
35 40 45

Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser Ser Thr Arg
50 55 60

Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu Lys Gly Glu
65 70 75 80

Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser Ser Ile Asp
85 90 95

Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser Leu Phe Val Glu
100 105 110

Asn Arg Leu Leu Glu Asp Ser Asn Ile Cys Asn Glu Thr Tyr Lys Lys
115 120 125

Arg Gln Leu Phe Arg Gly Asn Arg Asp Gly Ser Gly Arg Thr Ser Gly

130 135 16U 100 PCT.ST25
140

Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser Asp His Gln
145 150 155 160

Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg Asn Leu Lys
165 170 175

Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr Val Leu Thr
180 185 190

Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys Leu Ser Lys
195 200 205

Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly Ser Leu Ser
210 215 220

Arg Thr His Pro Pro Leu Glu Ser Thr Pro Leu Val Ser Gly Val Ala
225 230 235 240

Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly Ile Gly Gly
245 250 255

Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro Leu Glu Ala
260 265 270

Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro His Thr Gly
275 280 285

Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr Asn Pro Pro
290 295 300

Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln Ser Gln Gln
305 310 315 320

Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln Val Gln
325 330 335

Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln Ser Val Gln
340 345 350

Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala Val Ser Phe
355 360 365

Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His Phe Pro Met
370 375 380

Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu Ser Arg Gln
385 390 395 400

Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val Tyr Pro Ser
405 410 415

Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val Ile Ala Ser
420 425 430

Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser Gly Pro Pro
435 440 445

160 100 PCT.ST25
 Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln Gly Phe Val
 450 455 460

Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr Pro Ser Gly
 465 470 475 480

Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met Ala Pro Val
 485 490 495

Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala Ala Gln Gln
 500 505 510

Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe Gln Gly Leu
 515 520 525

Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile Asn Asn Gln
 530 535 540

Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro Thr Met Ser
 545 550 555 560

Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu Pro Gln Gln
 565 570 575

Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly Gln Gly Ser
 580 585 590

Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr Pro Pro Thr
 595 600 605

Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro Ser Ser Thr
 610 615 620

Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala Ser Met Ser
 625 630 635 640

Asn Ala Gly Trp Gln Val Lys Phe
 645

<210> 55
 <211> 651
 <212> PRT
 <213> Homo sapien

<400> 55

Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp Phe
 1 5 10 15

Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser Ser
 20 25 30

Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu Asp
 35 40 45

His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr Ser
 50 55 60

Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp Glu
 65 70 75 80

16U 100 PCT.ST25

Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn Ser
85 90 95

Ser Ile Asp Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser Leu
100 105 110

Phe Val Glu Asn Arg Leu Leu Glu Asp Ser Asn Ile Cys Asn Glu Thr
115 120 125

Tyr Lys Lys Arg Gln Leu Phe Arg Gly Asn Arg Asp Gly Ser Gly Arg
130 135 140

Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys Trp Ser
145 150 155 160

Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser Asn Arg
165 170 175

Asn Leu Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly Ile Thr
180 185 190

Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr Gly Lys
195 200 205

Leu Ser Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser Ser Gly
210 215 220

Ser Leu Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu Val Ser
225 230 235 240

Gly Val Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu Asn Gly
245 250 255

Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu Leu Pro
260 265 270

Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu Asn Pro
275 280 285

His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala Ile Tyr
290 295 300

Asn Pro Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val Gly Gln
305 310 315 320

Ser Gln Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro Gln Gln
325 330 335

Gln Val Gln Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val Thr Gln
340 345 350

Ser Val Gln Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr Pro Ala
355 360 365

Val Ser Phe Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr Gln His
370 375 380

Phe Pro Met Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met Thr Leu
385 390 395 400

160 100 PCT.ST25

Ser Arg Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly Pro Val
405 410 415

Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser Tyr Val
420 425 430

Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser Gly Ser
435 440 445

Gly Pro Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser Pro Gln
450 455 460

Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr Tyr Tyr
465 470 475 480

Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg Pro Met
485 490 495

Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro Gln Ala
500 505 510

Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln Gly Phe
515 520 525

Gln Gly Leu Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn Val Ile
530 535 540

Asn Asn Gln Gln Gly Thr Pro Val Gln Ser Val Met Val Ser Tyr Pro
545 550 555 560

Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln Gly Leu
565 570 575

Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln Ala Gly
580 585 590

Gln Gly Ser Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn Val Thr
595 600 605

Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His Cys Pro
610 615 620

Ser Ser Thr Val Pro Val Met Ser Ala Ser Cys Arg Thr Asn Cys Ala
625 630 635 640

Ser Met Ser Asn Ala Gly Trp Gln Val Lys Phe
645 650

<210> 56
<211> 89
<212> PRT
<213> Homo sapien

<400> 56

Met Ser Glu Gln Gly Asp Leu Asn Gln Ala Ile Ala Glu Glu Gly Gly
1 5 10 15

Thr Glu Gln Glu Thr Ala Thr Pro Glu Asn Gly Ile Val Lys Ser Glu
20 25 30

16U 100 PCT.ST25

Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
 35 40 45

Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
 50 55 60

Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Pro Gly
 65 70 75 80

Gly Glu Ser Leu Gln Asp Gln Thr Leu
 85

<210> 57
 <211> 88
 <212> PRT
 <213> Mus musculus

<400> 57

Met Ser Glu Gln Gly Gly Leu Thr Pro Thr Ile Leu Glu Glu Gly Gln
 1 5 10 15

Thr Glu Pro Glu Ser Ala Pro Glu Asn Gly Ile Leu Lys Ser Glu Ser
 20 25 30

Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Ala Ala Gln
 35 40 45

Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys Leu
 50 55 60

Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ser Ala Arg Ser Gly Gly
 65 70 75 80

Glu Ser His Gln Asp Gln Thr Leu
 85

<210> 58
 <211> 4462
 <212> DNA
 <213> homo sapien

<220>
 <221> CDS
 <222> (1336)..(2163)
 <223>

<400> 58
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 aatttttagtg acacactcat ttctactcga aacatttgcc tcattttcca tgatggacta 120
 ttttctaata caccacaat atttcctaga ttccctagtg cagttcccta agtgtgcca 180
 aatccccag cctgttagtg ttacttgta tttaagcaaa atgattcaaa tcatcatttg 240
 atacatgatg gaaatcccag gctcactcac caaatttcta gcaaatttg tgtgtgcttg 300
 taagggggat gggagggcag gagaaggcct tgtatttctt ctatgcatta caagctagtg 360
 gtttttcttc ctacgtcttg aacttactcc ttgcacatac ctttttctgc actgtgccat 420
 catccacttc tctttacttc ctaactacca ccaactgaaa attatacata taaaagcttt 480
 aaacaaagtc tcttgaggct ctcaaggag tttacattac agtatagttc agcaacaat 540
 tttaaatcaa atagtacacc tctttattct tagaattccc tctgccaaa aagaaatcag 600

16U 100 PCT.ST25

ctactttttt ttaaattcaa ggtccaactt tctgttgtgt tgctgattct ctctctcttt	660
tttccaacga ctccacttc tctctctagt ttacatgtct ccaaacctta agcctctgtt	720
aatactttca caataagtca attttgccaa cggtttgcct cccctagacc atctaggctg	780
ggcccagaac acctcatctt cactcccact gaagtgttcc tgaaggtcag ctctcactga	840
ccttgattct gctcccctac actgtcacca gaagctatcc acctatggtt ctaattcagt	900
aagtccaact ctctcacccc ctttttttgt ctcagctgtg tgggctttcc caggatggca	960
tgcaatggga cccctgtgcc atgcatattg taaaggaaaa tgctccctc catgcgctac	1020
aaaaacgac atttatgatg gcactttgaa aagatatggg ttgtggtgtc acatattgac	1080
aattccttgg ccagaggctt aacagtgcc aagtgccag aagattaaga agacagcaaa	1140
aacagaaaag ggagaagatg gtgaagtagt tatataacat gagcgagaat gtcctgatt	1200
acaaagcaga gaaattgact ttttttctta gtgttttcta tagtcattgc tctatccctg	1260
ttctagaatt caagtcatga taagaatttc ttcacgttga cttcctgcat tgctttcaga	1320
cattgcaatt aaaga atg cga aga aag aac ctc aca gag gta aca gag ttt	1371
Met Arg Arg Lys Asn Leu Thr Glu Val Thr Glu Phe	
1 5 10	
gtt ttc ctg gga ttc tcc aga ttc cac aaa cat cac atc act ctc ttt	1419
Val Phe Leu Gly Phe Ser Arg Phe His Lys His His Ile Thr Leu Phe	
15 20 25	
gtg gtt ttt ctc atc ctg tac aca tta act gtg gct ggc aat gcc atc	1467
Val Val Phe Leu Ile Leu Tyr Thr Leu Thr Val Ala Gly Asn Ala Ile	
30 35 40	
atc atg acc atc atc tgc att gac cgt cac ctc cac act ccc atg tac	1515
Ile Met Thr Ile Ile Cys Ile Asp Arg His Leu His Thr Pro Met Tyr	
45 50 55 60	
ttc ttc ctg agc atg ctg gct agc tca aag aca gtg tac aca ctg ttc	1563
Phe Phe Leu Ser Met Leu Ala Ser Ser Lys Thr Val Tyr Thr Leu Phe	
65 70 75	
atc att cca cag atg ctc tcc agc ttc gta acc cag acc cag cca atc	1611
Ile Ile Pro Gln Met Leu Ser Ser Phe Val Thr Gln Thr Gln Pro Ile	
80 85 90	
tcc cta gca ggt tgt acc acc caa acg ttc ttc ttt gtt acc ttg gcc	1659
Ser Leu Ala Gly Cys Thr Thr Gln Thr Phe Phe Phe Val Thr Leu Ala	
95 100 105	
atc aac aat tgc ttc ttg ctc aca gtg atg ggc tat gac cac tat atg	1707
Ile Asn Asn Cys Phe Leu Leu Thr Val Met Gly Tyr Asp His Tyr Met	
110 115 120	
gcc atc tgc aat ccc ttg aga tac agg gtc att acg agc aag aag gtg	1755
Ala Ile Cys Asn Pro Leu Arg Tyr Arg Val Ile Thr Ser Lys Lys Val	
125 130 135 140	
tgt gtc cag ctg gtg tgt gga gcc ttt agc att ggc ctg gcc atg gca	1803
Cys Val Gln Leu Val Cys Gly Ala Phe Ser Ile Gly Leu Ala Met Ala	
145 150 155	
gct gtc cag gta aca tcc ata ttt acc tta cct ttt tgt cac acg gtg	1851
Ala Val Gln Val Thr Ser Ile Phe Thr Leu Pro Phe Cys His Thr Val	
160 165 170	
gtt ggt cat ttc ttc tgt gac atc ctc cct gtc atg aaa ctc tcc tgt	1899
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16U 100 PCT.ST25

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16U 100 PCT.ST25
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